



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 09:25 PM UTC

PDB ID : 7K0T / pdb_00007k0t
EMDB ID : EMD-22616
Title : Cryo-EM structure of rabbit RyR1 in the presence of AMP-PCP in nanodisc
Authors : Nayak, A.R.; Samso, M.
Deposited on : 2020-09-05
Resolution : 4.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

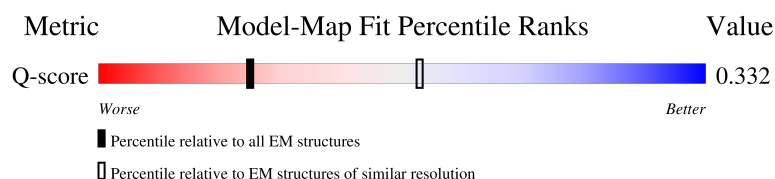
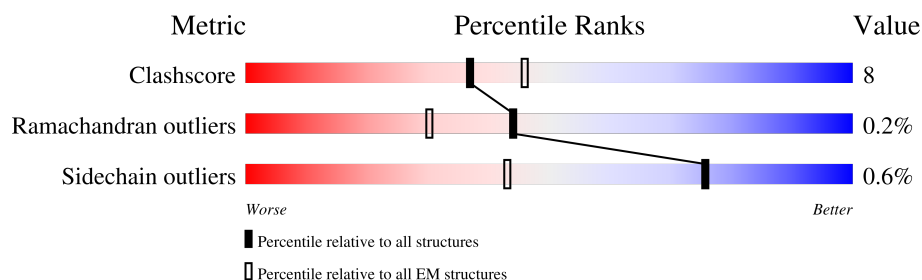
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	5037	 69% 13% 19%
1	B	5037	 69% 12% 19%
1	C	5037	 70% 12% 19%
1	D	5037	 69% 12% 19%

2 Entry composition [i](#)

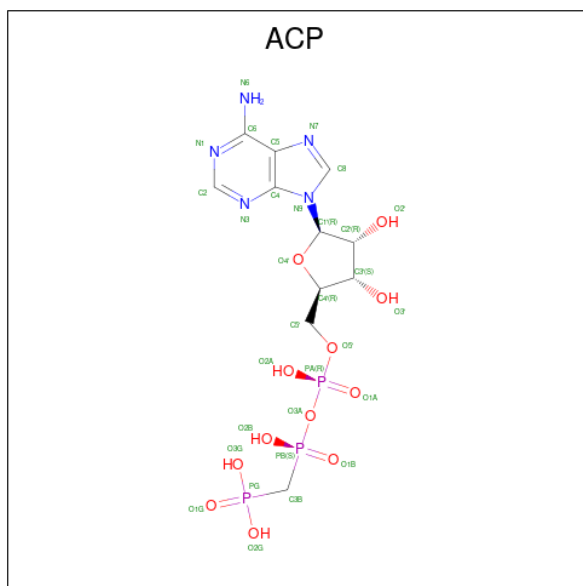
There are 3 unique types of molecules in this entry. The entry contains 115905 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called RyR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4105	Total	C	N	O	S	0	0
			28962	18349	5127	5329	157		
1	B	4105	Total	C	N	O	S	0	0
			28934	18331	5126	5320	157		
1	D	4105	Total	C	N	O	S	0	0
			28933	18332	5125	5319	157		
1	C	4105	Total	C	N	O	S	0	0
			28948	18340	5129	5322	157		

- Molecule 2 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	11	5	12	3	
2	B	1	Total	C	N	O	P	0
			31	11	5	12	3	

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Mol	Chain	Residues	Atoms					AltConf
2	D	1	Total	C	N	O	P	0
			31	11	5	12	3	
2	C	1	Total	C	N	O	P	0
			31	11	5	12	3	

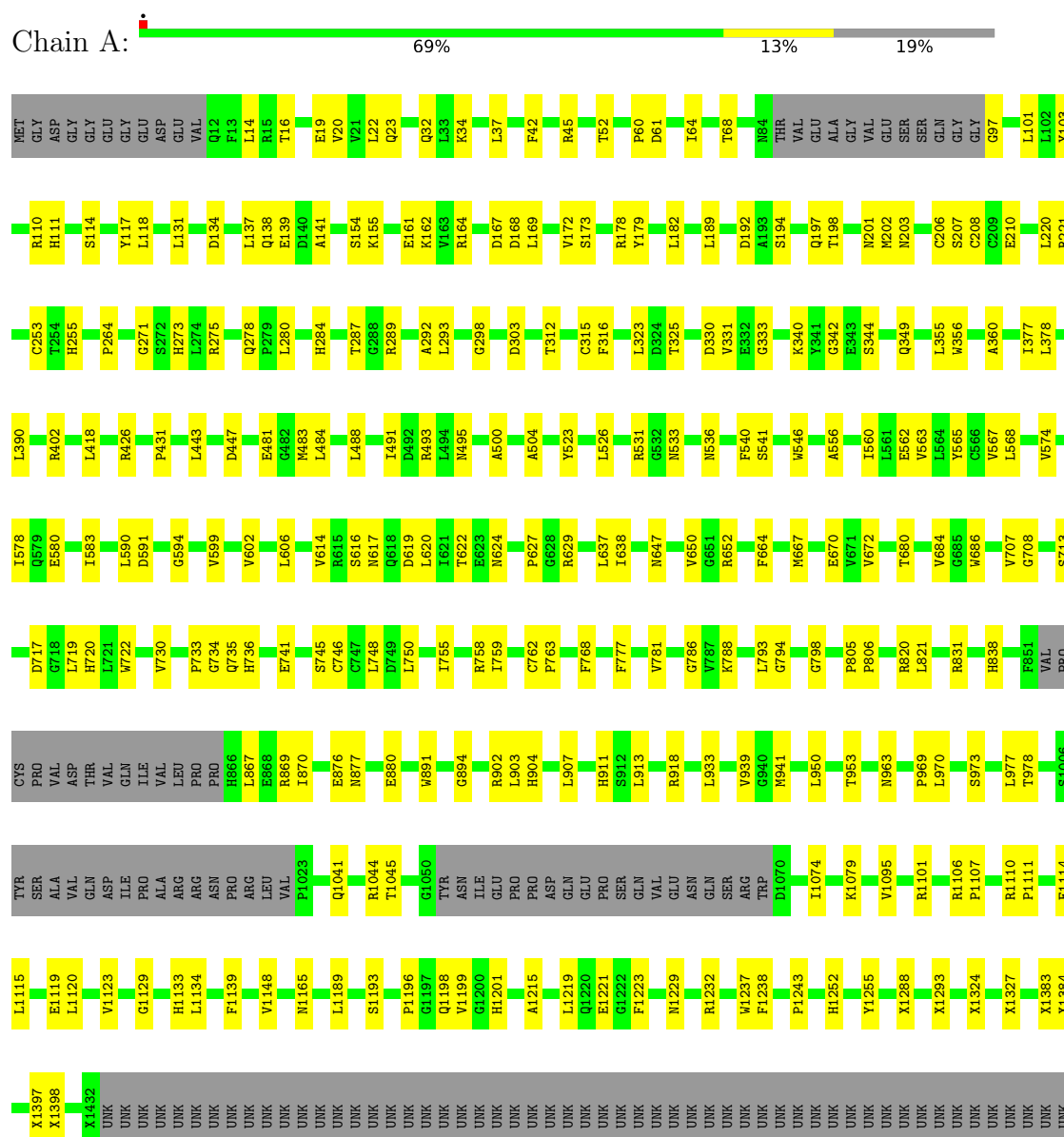
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: RyR1









Chain D: 69% 12% 19%









L4884	D4744	SER	PRO	ASP	PRO	D4744	GLY	LEU	P4106	K3999
K4887	F4780	TRP	GLU	MET	PRO	F4780	GLY	TRP	Q4109	A4004
R4892	I4783	SER	PRO	ASP	PRO	I4783	ALA	VAL	Q4005	D4006
P4904	D4786	GLY	LYS	THR	LYS	D4786	ALA	ARG	Q4133	Q4009
R4913	Y4791	ALA	LYS	PRO	LYS	Y4791	ALA	ASP	D4138	I4010
E4942	Y4794	GLY	ALA	ALA	ALA	Y4794	GLY	GLY	N4142	L4013
R4944	Y4795	GLY	PRO	THR	PRO	Y4795	GLY	GLY	R4159	L4016
V4950	M4786	ASP	ALA	GLU	ALA	M4786	GLY	THR	L4017	L4016
M4798	V4797	GLU	LYS	GLY	LYS	V4797	ALA	VAL	E4182	E4018
S4799	M4798	GLU	LYS	GLY	LYS	M4798	ALA	ALA	I4183	L4019
C4958	S4799	GLU	GLU	PRO	GLU	S4799	GLY	ALA	M4184	Q4020
D4966	H4812	L4626	ALA	ILE	GLY	H4812	GLY	ALA	I4190	K4021
H4978	D4815	L4632	GLY	LEU	ALA	D4815	ALA	THR	M4023	D4022
H4983	I4816	A4654	GLY	LYS	GLY	I4816	ALA	ALA	M4024	M4023
V4984	T4822	Y4661	GLY	VAL	GLY	T4822	GLY	ASP	V4025	V4025
L4985	I4826	L4664	ASP	ASP	F4540	I4826	ALA	SER	L4030	L4030
I4996	L4827	K4665	GLY	GLY	R4563	L4827	ALA	LEU	I4218	N4034
K4998	S4828	V4666	GLU	GLU	R4563	S4828	ARG	PHE	V4222	I4040
D4999	T4831	L4668	GLU	GLU	L4567	T4831	ALA	GLY	E4227	D4046
E5000	V4848	R4673	GLU	LEU	N4574	V4848	GLY	GLY	E4229	M4047
T5001	T4852	R4679	VAL	VAL	L4577	T4852	GLU	VAL	C4238	S4051
H5003	V4853	K4680	PRO	PRO	L4578	V4853	GLY	GLY	E4239	T4058
H5013	A4855	I4688	PRO	PRO	K4581	A4855	ALA	ALA	D4240	F4062
R5017	F4859	T4689	PRO	PRO	P4587	F4859	GLY	LYS	I4242	F4062
C5018	Y4863	E4690	GLY	GLY	GLY	Y4863	VAL	VAL	E4253	F4065
S5037	K4864	Q4691	ASP	PRO	GLU	K4864	ARG	ARG	PRO	K4069
	S4866	V4697	ASP	PRO	GLU	S4866	THR	THR	GLY	K4069
	E4867	K4698	MET	PRO	ASP	E4867	VAL	VAL	GLY	V4072
	D4868	G4699	GLY	PRO	MET	D4868	GLU	GLU	ARG	F4077
	E4869	R4703	LYS	GLY	GLY	E4869	LEU	LEU	GLU	F4077
	D4870	L4704	ALA	ASP	ALA	D4870	ALA	ARG	ALA	Q4078
	E4871	V4705	ASP	GLY	ALA	E4871	ASP	ARG	ASP	D4079
	P4872	L4706	GLY	GLY	GLY	P4872	LEU	LEU	GLU	Y4080
	D4873	M4707	ASP	GLY	GLY	D4873	PRO	THR	ASP	V4081
	M4874	T4708	LEU	ASN	ASP	M4874	ALA	ASP	GLY	I4088
	K4875	Y4715	ALA	GLY	LEU	K4875	THR	ARG	GLY	Q4094
	D4877	W4716	GLY	LYS	ALA	D4877	SER	GLY	GLY	Q4094
	M4878	I4731	ALA	GLY	ALA	M4878	GLY	ALA	ALA	V4097
	M4879	I4731	SER	GLY	GLY	M4879	VAL	THR	ALA	K4101
	C4882	T4737	GLY	VAL	GLY	C4882	LEU	LEU	ALA	Q4102
	Y4883	A4738	GLY	PRO	GLY	Y4883	ALA	ALA	GLY	Q4102
			GLY	ALA	ALA		LEU	GLN	GLY	F4103
									ALA	G4105

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	21551	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70.3	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.128	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	462.24002, 462.24002, 462.24002	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACP, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.16	0/25009	0.41	4/33951 (0.0%)
1	B	0.18	1/24980 (0.0%)	0.44	8/33913 (0.0%)
1	C	0.17	0/24994	0.42	3/33929 (0.0%)
1	D	0.17	1/24979 (0.0%)	0.42	5/33913 (0.0%)
All	All	0.17	2/99962 (0.0%)	0.42	20/135706 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	889	GLN	C-N	8.94	1.46	1.33
1	B	967	PRO	C-N	7.42	1.49	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	967	PRO	O-C-N	11.34	136.92	122.86
1	D	4872	PRO	N-CA-C	-9.10	102.24	113.98
1	B	4868	ASP	CB-CA-C	7.78	120.52	109.71
1	A	4690	GLU	CA-C-N	7.59	130.94	120.39
1	A	4690	GLU	C-N-CA	7.59	130.94	120.39

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	883	ALA	Peptide
1	D	889	GLN	Mainchain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	28962	0	24423	420	0
1	B	28934	0	24389	415	0
1	C	28948	0	24429	399	0
1	D	28933	0	24401	416	0
2	A	31	0	14	6	0
2	B	31	0	14	4	0
2	C	31	0	14	7	0
2	D	31	0	14	5	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	115905	0	97698	1631	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 1631 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4662:ASN:O	1:B:4666:VAL:HG11	1.38	1.23
1:B:3758:MET:HE2	1:B:3758:MET:HA	1.29	1.11
1:D:4662:ASN:O	1:D:4666:VAL:HG11	1.52	1.09
1:C:4865:LYS:HE2	1:C:4865:LYS:HA	1.37	1.06
1:D:3674:ILE:HB	1:D:3769:ARG:HH21	1.19	1.04

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	3172/5037 (63%)	2945 (93%)	222 (7%)	5 (0%)	43	77
1	B	3172/5037 (63%)	2926 (92%)	240 (8%)	6 (0%)	43	77
1	C	3172/5037 (63%)	2921 (92%)	246 (8%)	5 (0%)	43	77
1	D	3172/5037 (63%)	2930 (92%)	238 (8%)	4 (0%)	48	83
All	All	12688/20148 (63%)	11722 (92%)	946 (8%)	20 (0%)	44	77

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4865	LYS
1	B	4875	LYS
1	B	4876	CYS
1	D	3771	HIS
1	B	1708	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2464/3264 (76%)	2451 (100%)	13 (0%)	81	81
1	B	2455/3264 (75%)	2436 (99%)	19 (1%)	73	77
1	C	2459/3264 (75%)	2440 (99%)	19 (1%)	73	77
1	D	2455/3264 (75%)	2444 (100%)	11 (0%)	84	82
All	All	9833/13056 (75%)	9771 (99%)	62 (1%)	76	80

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4875	LYS
1	C	4868	ASP
1	D	3762	ARG
1	C	4867	GLU
1	C	4884	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 117 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	12	GLN
1	C	3895	HIS
1	D	2193	GLN
1	C	3814	GLN
1	C	1220	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACP	A	5101	-	31,33,33	1.66	8 (25%)	47,52,52	1.86	10 (21%)
2	ACP	C	5101	-	31,33,33	1.66	8 (25%)	47,52,52	1.83	10 (21%)
2	ACP	D	5101	-	31,33,33	1.66	8 (25%)	47,52,52	1.84	10 (21%)
2	ACP	B	5101	-	31,33,33	1.66	8 (25%)	47,52,52	1.85	10 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACP	A	5101	-	-	4/19/38/38	0/3/3/3
2	ACP	C	5101	-	-	2/19/38/38	0/3/3/3
2	ACP	D	5101	-	-	2/19/38/38	0/3/3/3
2	ACP	B	5101	-	-	2/19/38/38	0/3/3/3

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	5101	ACP	C5-C4	4.74	1.47	1.39
2	A	5101	ACP	C5-C4	4.72	1.47	1.39
2	C	5101	ACP	C5-C4	4.72	1.47	1.39
2	B	5101	ACP	C5-C4	4.70	1.47	1.39
2	A	5101	ACP	PG-O2G	2.92	1.61	1.55

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5101	ACP	C5-C4-N3	-5.85	118.66	126.72
2	B	5101	ACP	C5-C4-N3	-5.84	118.68	126.72
2	C	5101	ACP	C5-C4-N3	-5.83	118.68	126.72
2	D	5101	ACP	C5-C4-N3	-5.82	118.71	126.72
2	D	5101	ACP	N3-C4-N9	4.61	135.01	127.17

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	5101	ACP	C3'-C4'-C5'-O5'
2	A	5101	ACP	O4'-C4'-C5'-O5'

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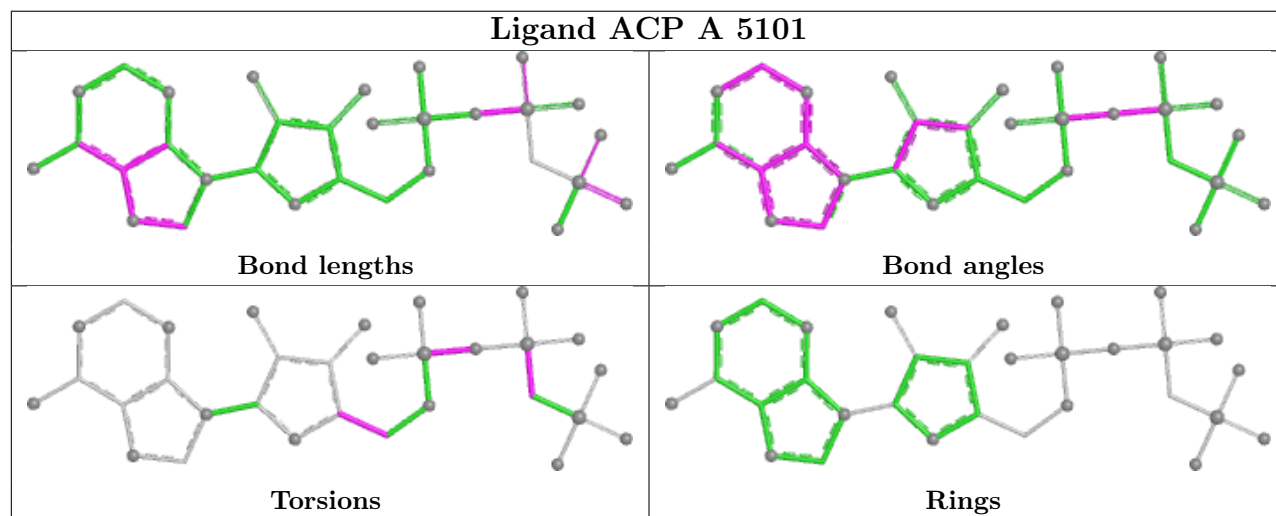
Mol	Chain	Res	Type	Atoms
2	B	5101	ACP	C3'-C4'-C5'-O5'
2	C	5101	ACP	C3'-C4'-C5'-O5'
2	D	5101	ACP	C3'-C4'-C5'-O5'

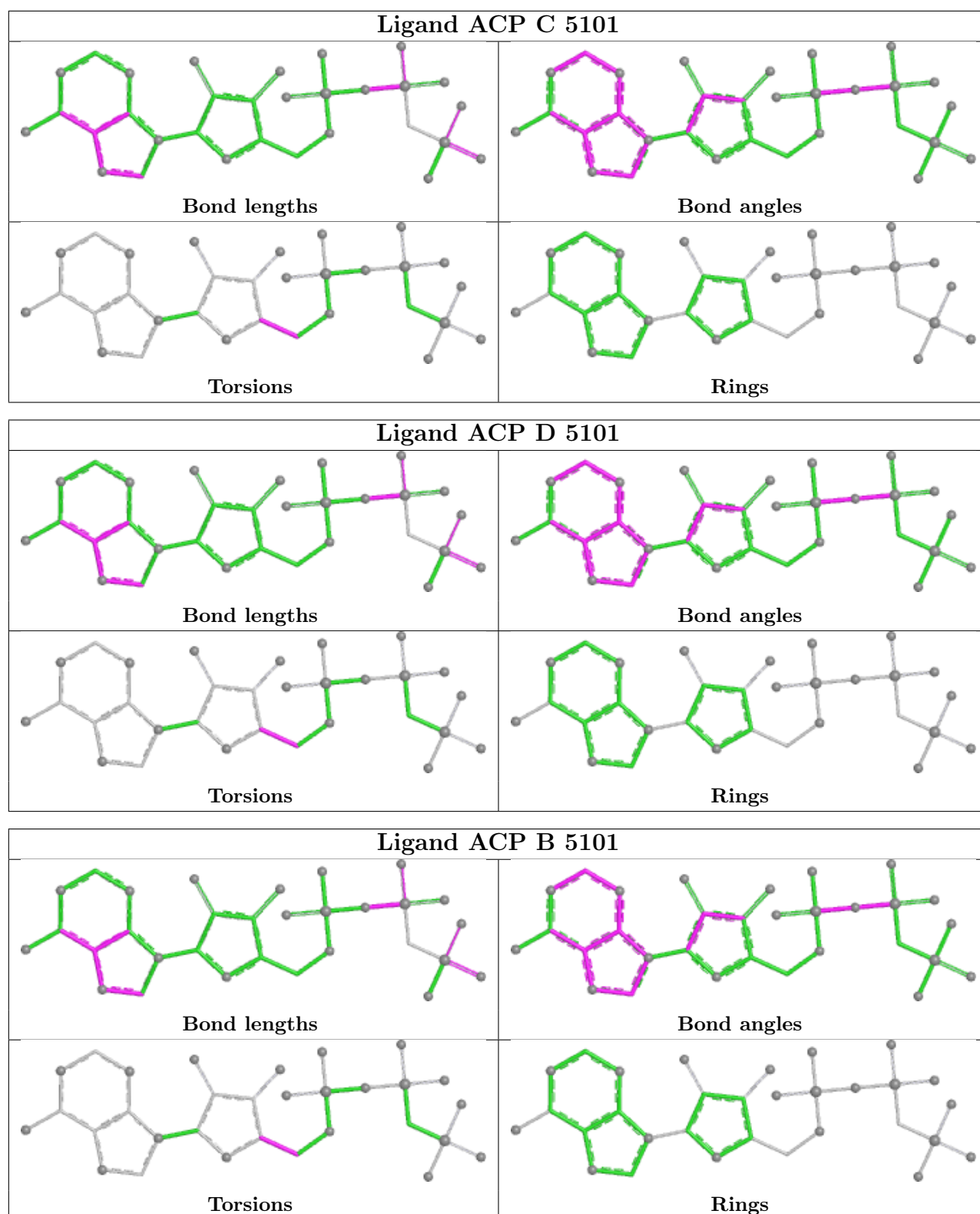
There are no ring outliers.

4 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5101	ACP	6	0
2	C	5101	ACP	7	0
2	D	5101	ACP	5	0
2	B	5101	ACP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	7
1	D	7
1	A	7
1	C	7

The worst 5 of 28 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3288:UNK	C	3289:UNK	N	19.38
1	B	3510:UNK	C	3511:UNK	N	17.00
1	D	3191:UNK	C	3192:UNK	N	16.39
1	D	3510:UNK	C	3511:UNK	N	15.09
1	D	3288:UNK	C	3289:UNK	N	14.70

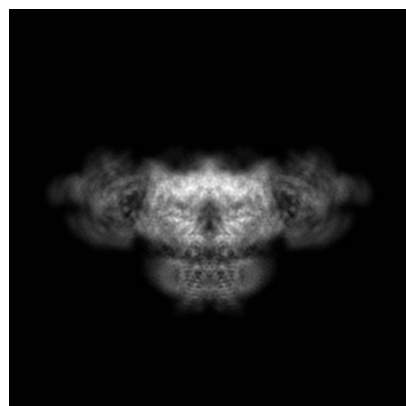
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22616. These allow visual inspection of the internal detail of the map and identification of artifacts.

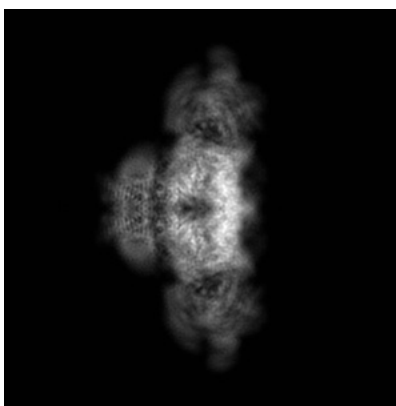
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

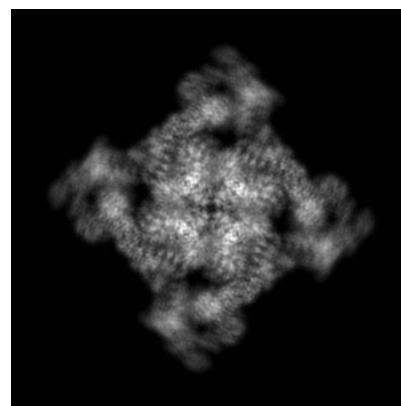
6.1.1 Primary map



X

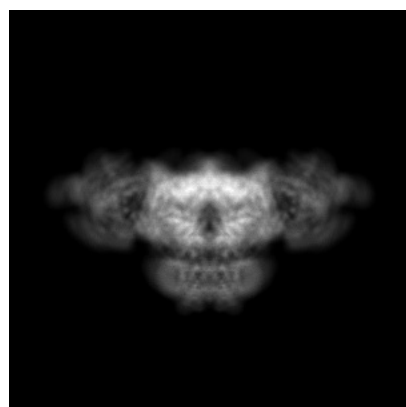


Y

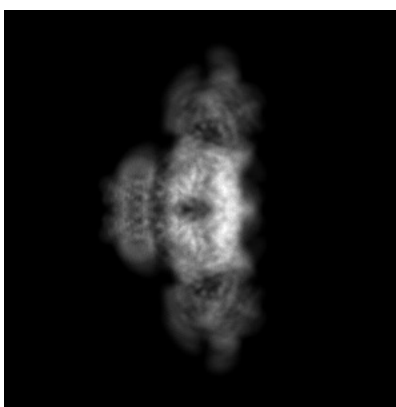


Z

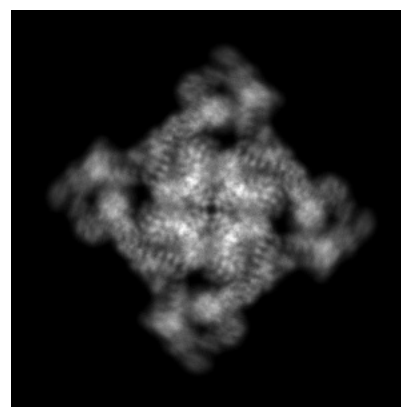
6.1.2 Raw map



X



Y

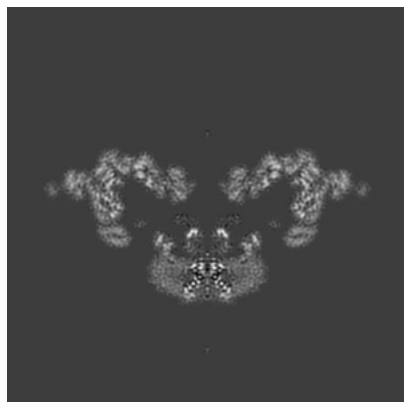


Z

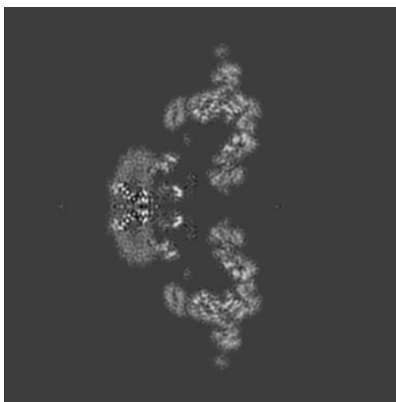
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

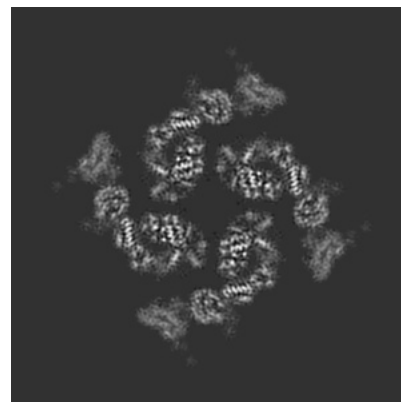
6.2.1 Primary map



X Index: 216

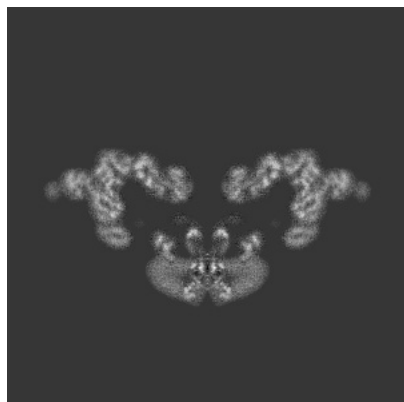


Y Index: 216

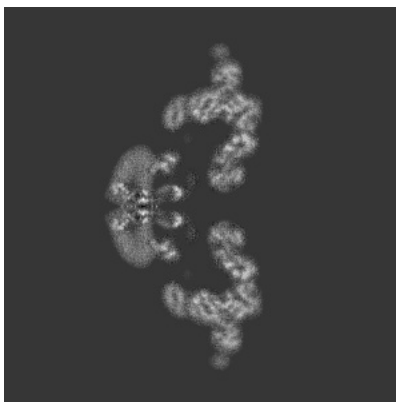


Z Index: 216

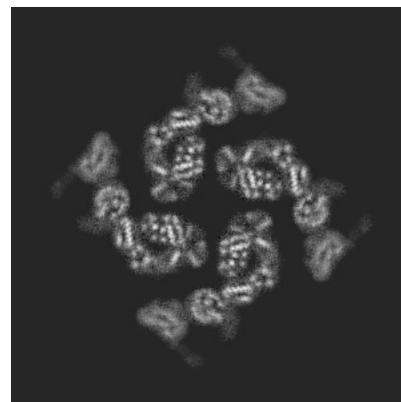
6.2.2 Raw map



X Index: 216



Y Index: 216

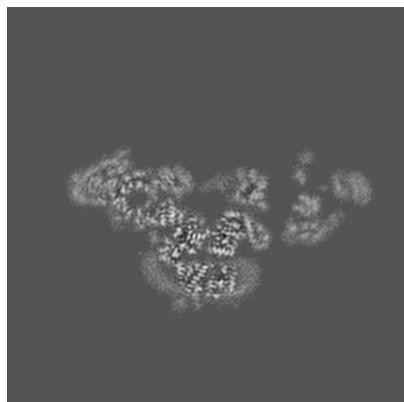


Z Index: 216

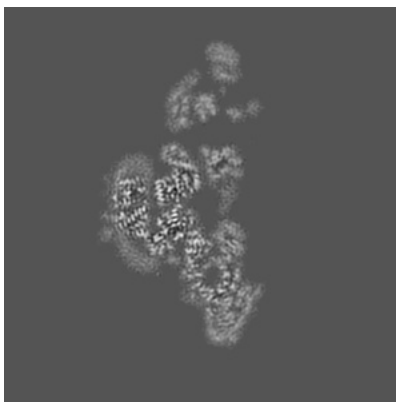
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

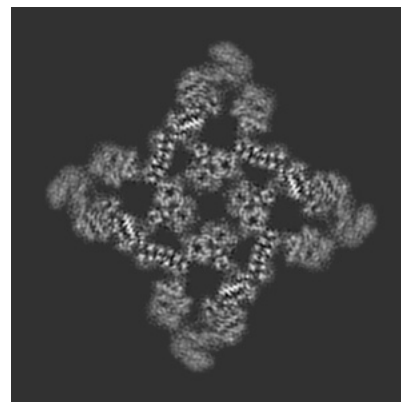
6.3.1 Primary map



X Index: 233

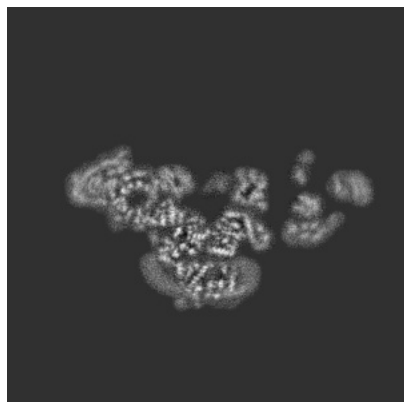


Y Index: 199

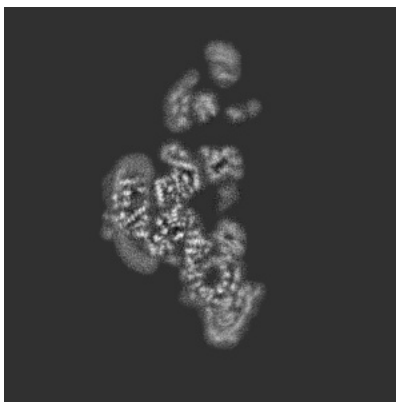


Z Index: 233

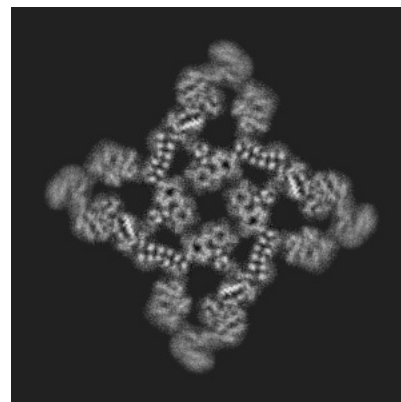
6.3.2 Raw map



X Index: 233



Y Index: 199

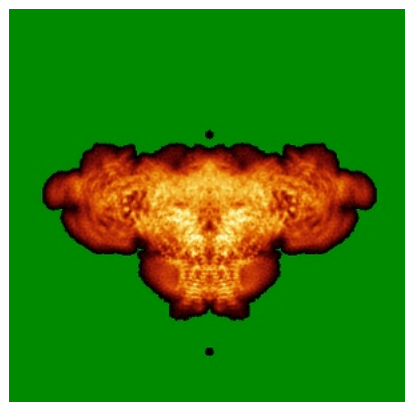


Z Index: 233

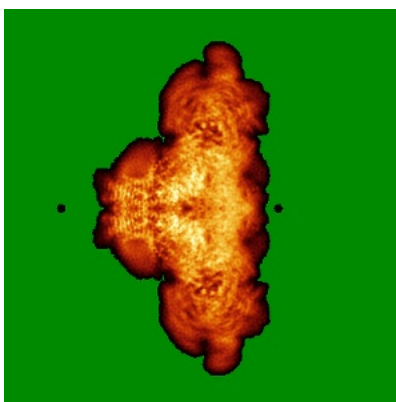
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

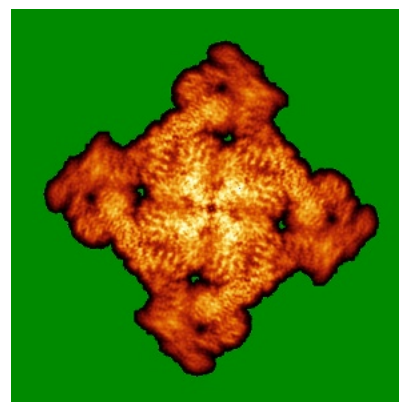
6.4.1 Primary map



X

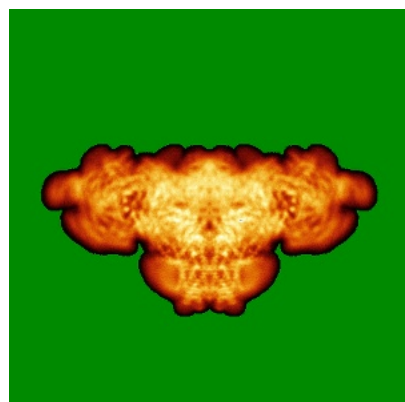


Y

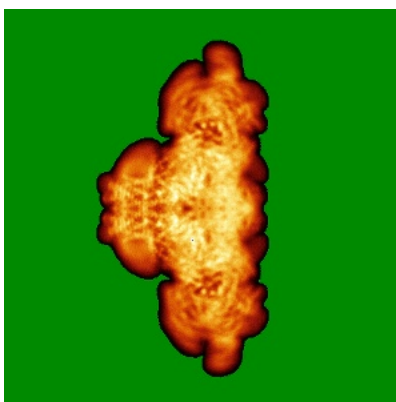


Z

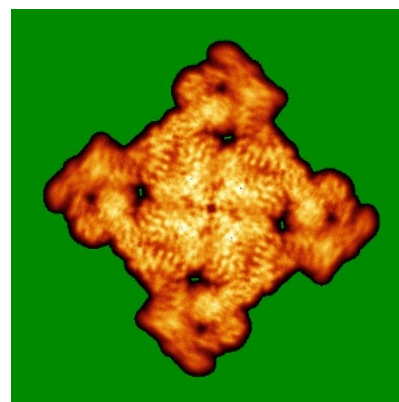
6.4.2 Raw map



X



Y

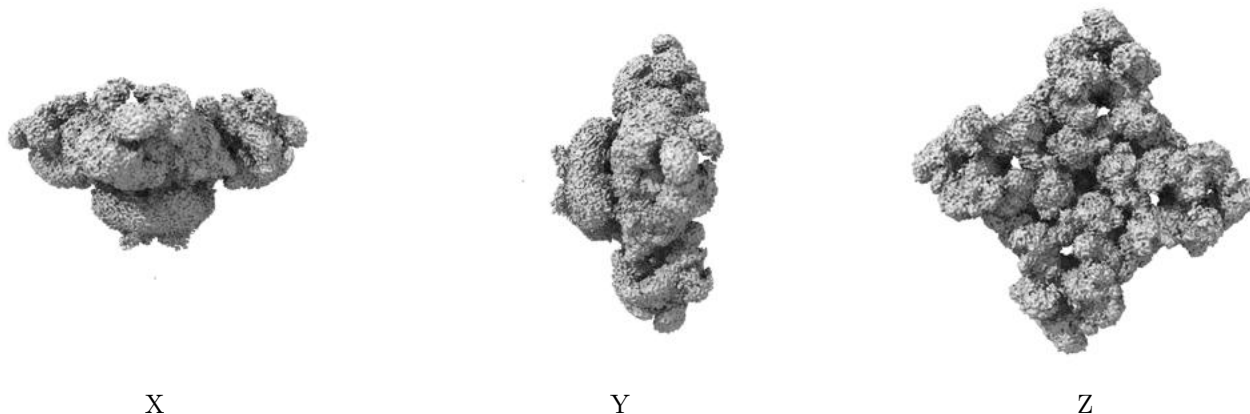


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

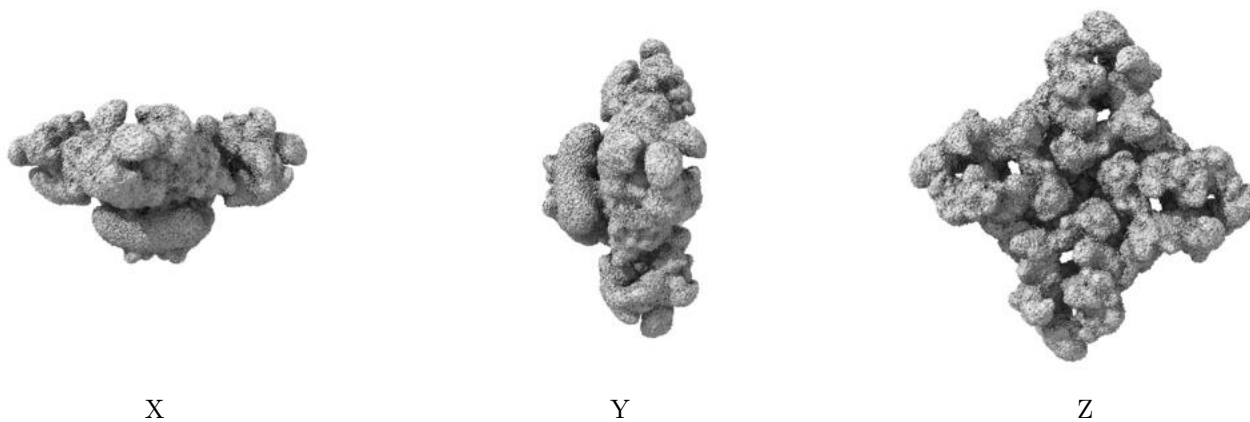
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

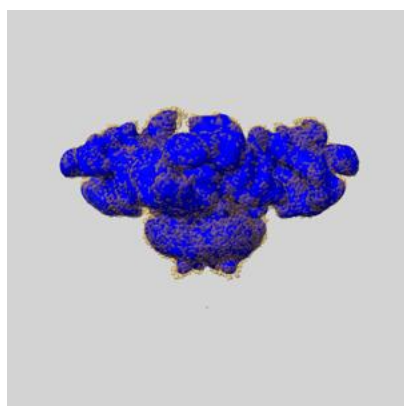
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

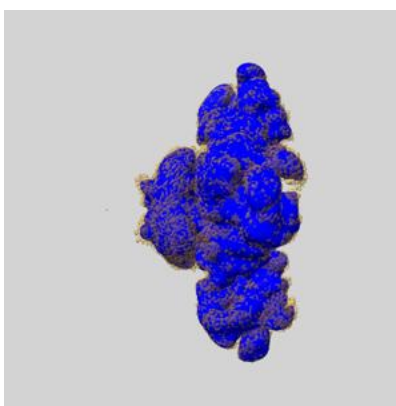
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

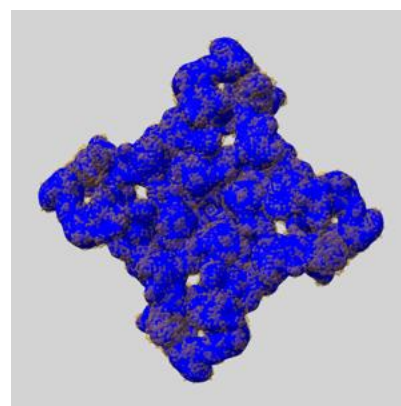
6.6.1 emd_22616_msk_1.map [i](#)



X



Y

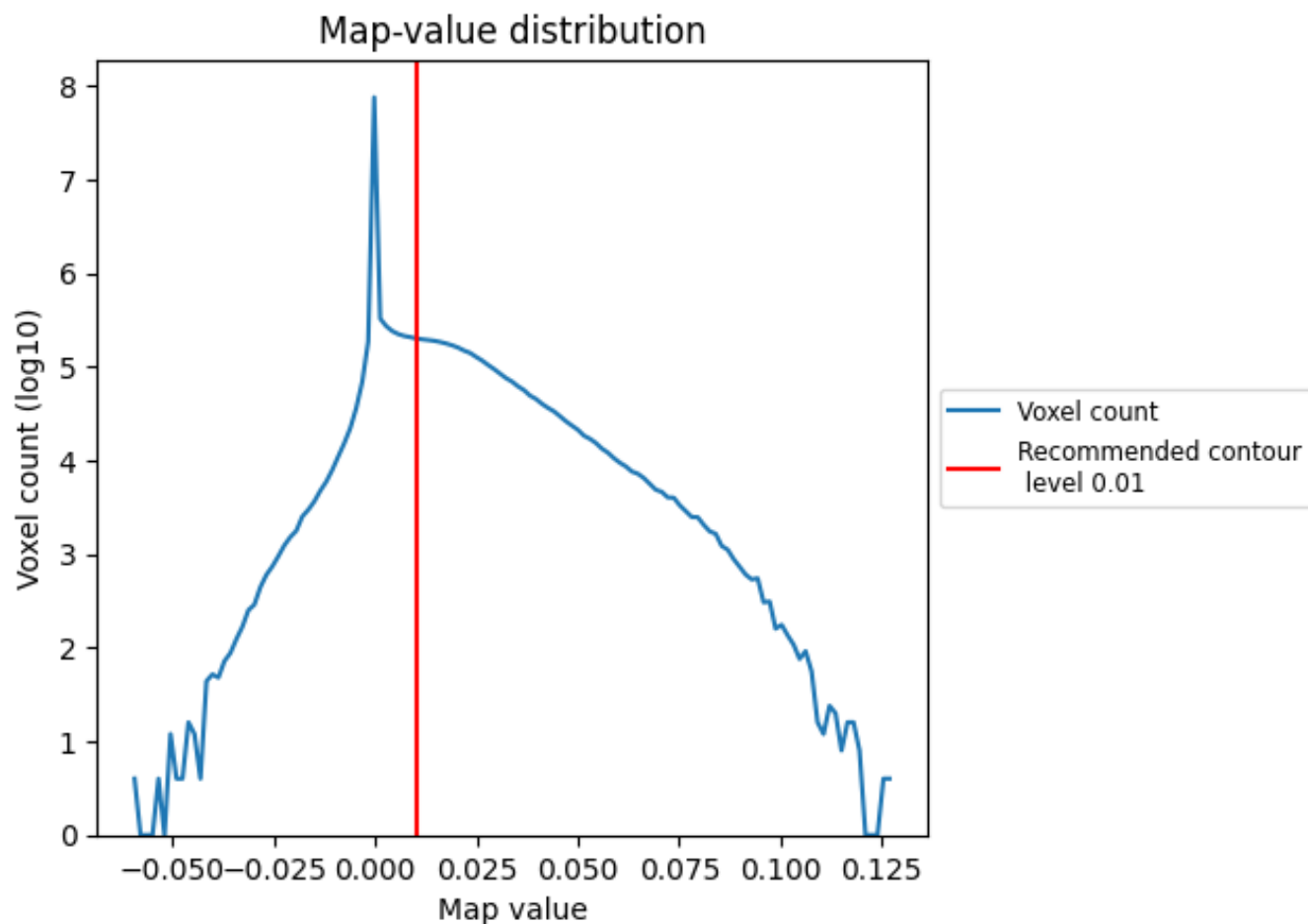


Z

7 Map analysis [i](#)

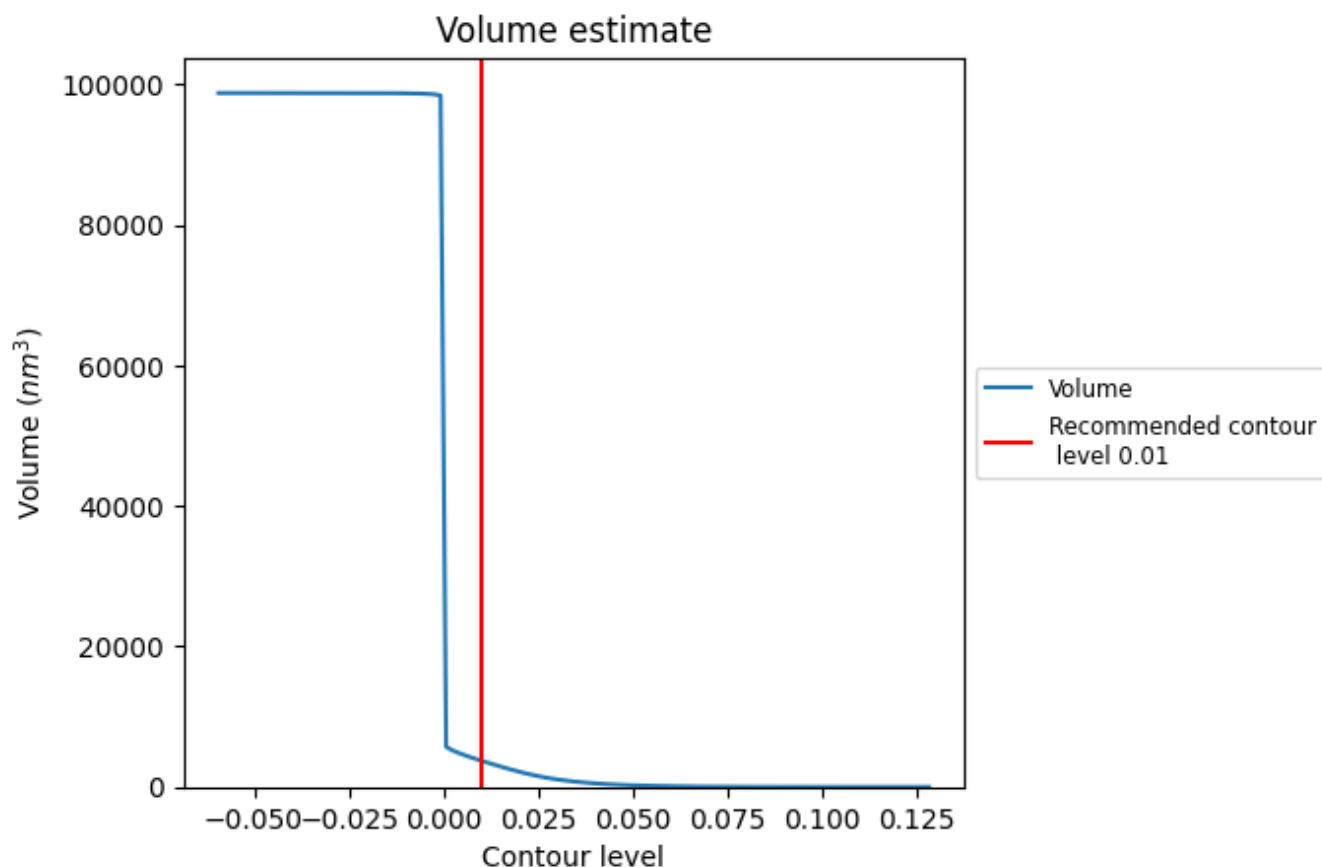
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

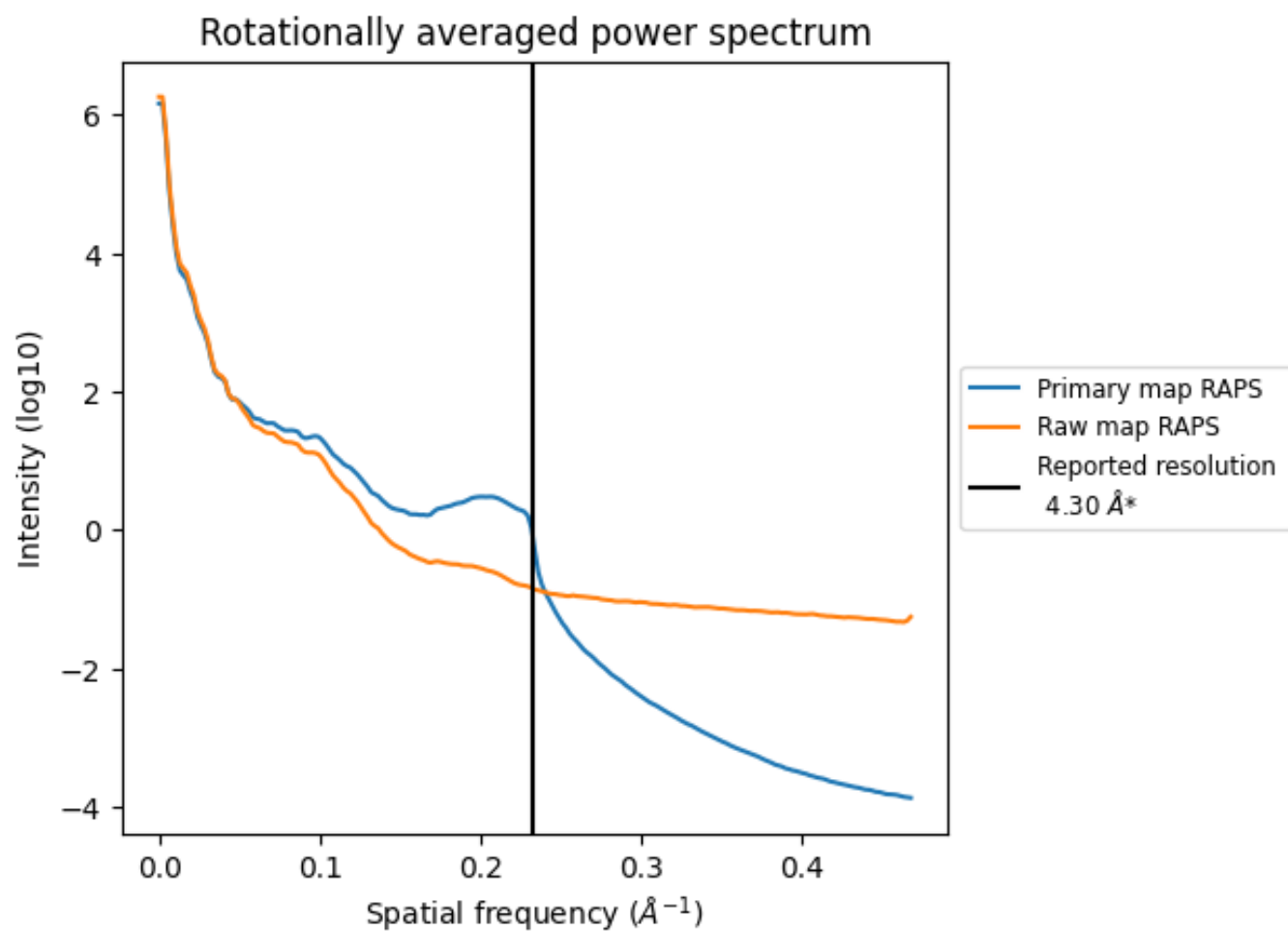
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3741 nm^3 ; this corresponds to an approximate mass of 3379 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

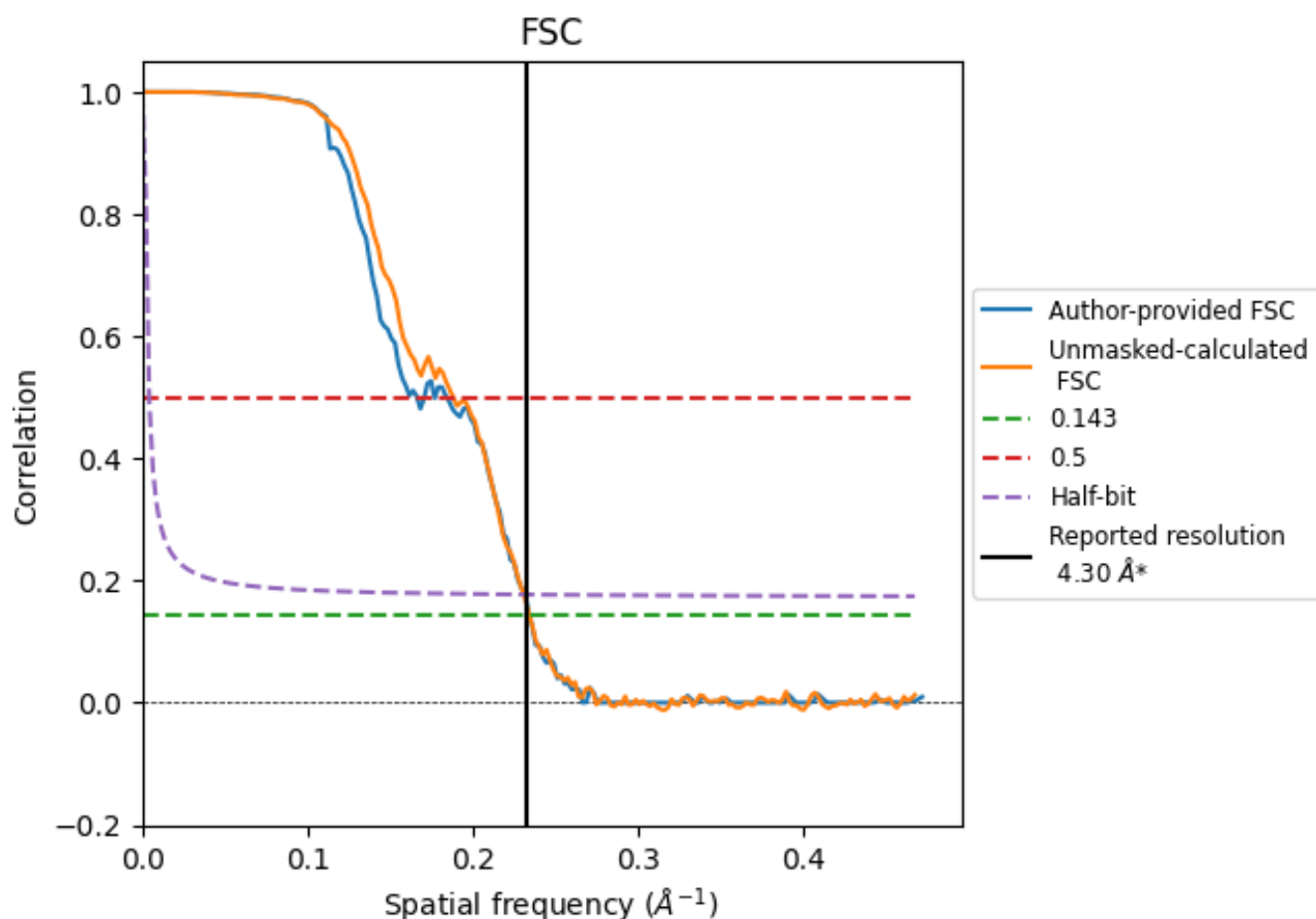


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.233 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

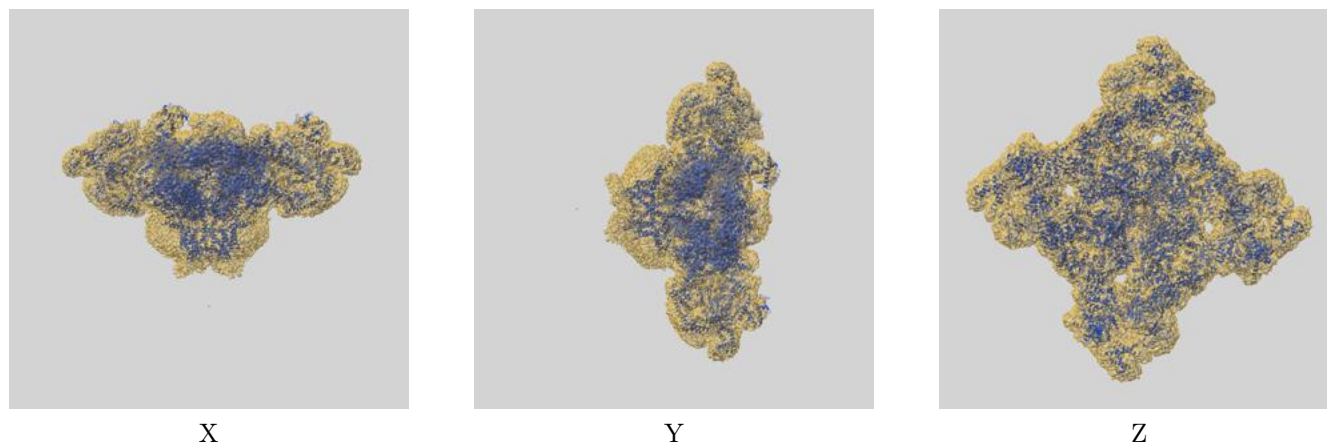
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.27	6.02	4.32
Unmasked-calculated*	4.27	5.31	4.33

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

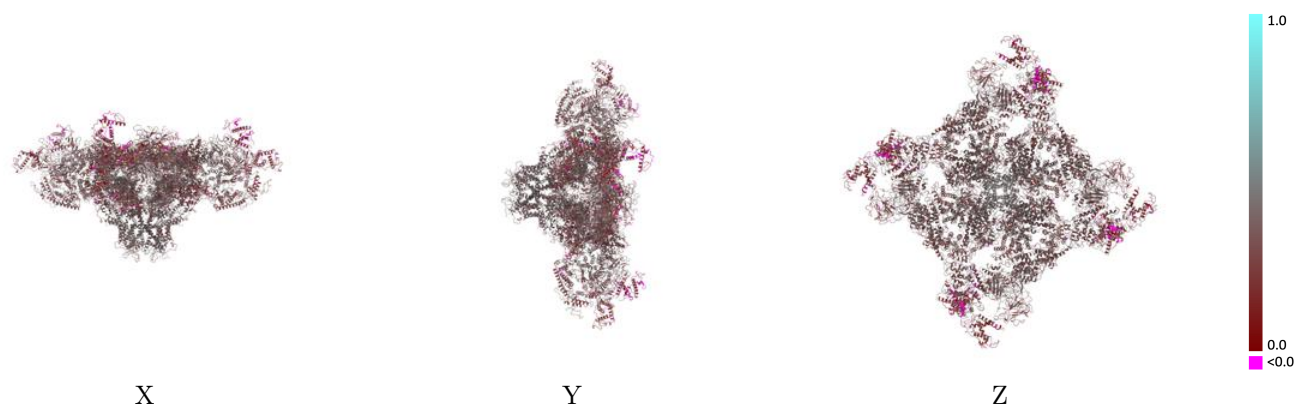
This section contains information regarding the fit between EMDB map EMD-22616 and PDB model 7K0T. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



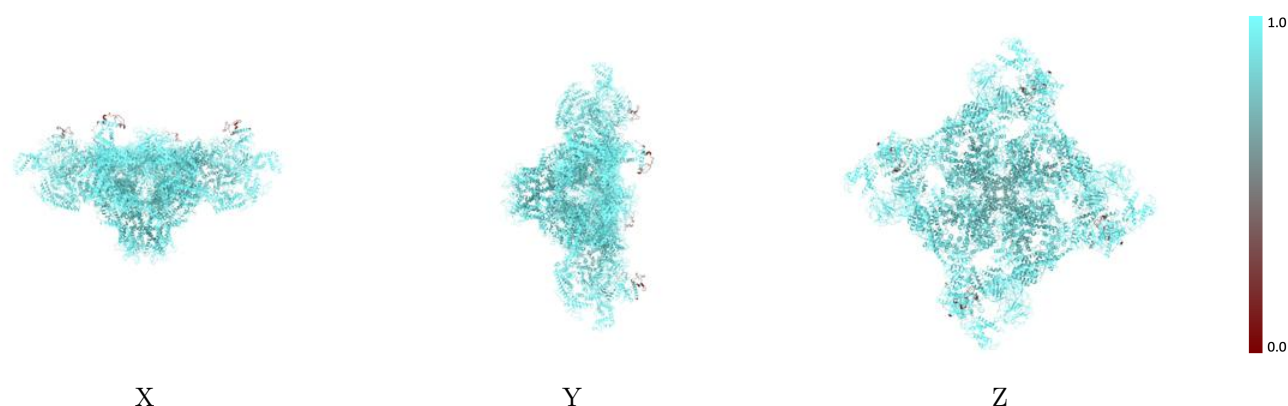
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



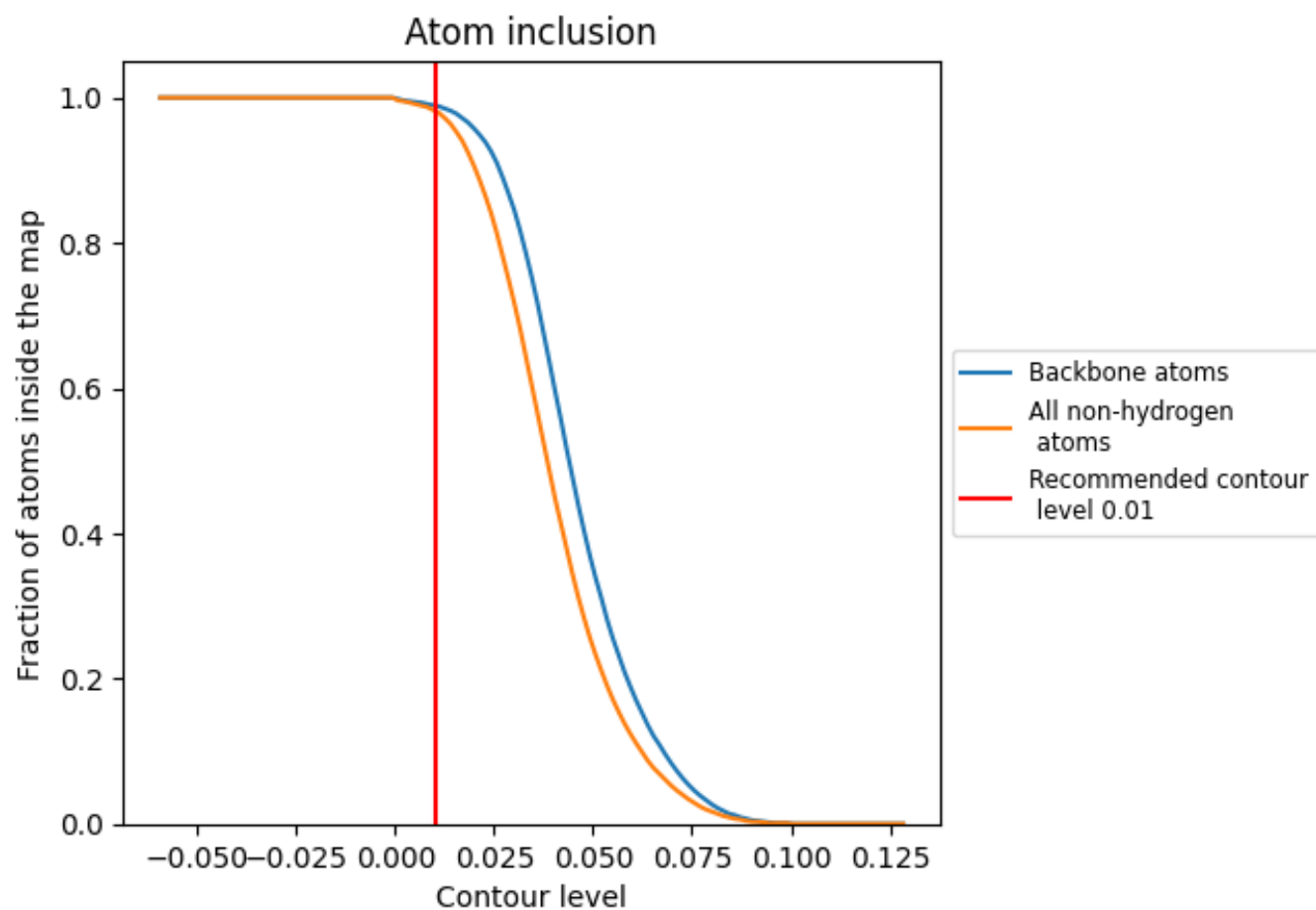
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9820	0.3320
A	0.9820	0.3320
B	0.9820	0.3310
C	0.9830	0.3320
D	0.9820	0.3320

